OM protein - nucleic search, using frame_plus_p2n model

                    GenCore version 5.1.6
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Run on:             June 23, 2004, 07:21:45 ; Search time 6975 Seconds
                                              (without alignments)
                                              4132.347 Million cell updates/sec

Title:
Perfect score:      665
Sequence:           US-10-029-345A-109
                    1 MAHEMIGTQIVTERLVALLE.........LGKVGSQSSFSGGSMEIIEVS 665

Searched:           3470272 seqs, 2167516995 residues

Scoring table:      OLIGO           Xgapext 60.0
                    Xgapop 60.0 ,   Xgapext 60.0
                    Ygapop 60.0 ,   Ygapext 60.0
                    Fgapop 6.0 ,    Fgapext 7.0
                    Delop 6.0 ,     Delext 7.0

Word size:          1419

Total number of hits satisfying chosen parameters:      0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10029345/runat_23062004_072139_16034/app_query.fasta_1.839
-DB=GenEmbl -QFMT=fastap -SUFFIX=oli2.rge -MINMATCH=0.1 -LOOPCt=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=75
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10029345 @CGN_1_1_4545 @runat_23062004_072139_16034 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :
            GenEmbl:*
        1:  gb_ba:*
        2:  gb_htg:*
        3:  gb_in:*
        4:  gb_om:*
        5:  gb_ov:*
        6:  gb_vi:*
        7:  gb_pat:*
        8:  gb_ph:*
        9:  gb_pl:*
       10:  gb_pr:*
       11:  gb_ro:*
       12:  gb_sts:*
       13:  gb_sy:*
       14:  gb_un:*
       15:  gb_vi:*
       16:  em_ba:*
       17:  em_fun:*
       18:  em_hum:*
       19:  em_in:*
       20:  em_mu:*
       21:  em_om:*
       22:  em_or:*
       23:  em_ov:*
       24:  em_pat:*
       25:  em_ph:*
       26:  em_pl:*
       27:  em_ro:*
       28:  em_sts:*
       28:  em_un:*

       29:  em_vi:*
       30:  em_htg_hum:*
       31:  em_htg_inv:*
       32:  em_htg_other:*
       33:  em_htg_mus:*
       34:  em_htg_pln:*
       35:  em_htg_rod:*
       36:  em_htg_mam:*
       37:  em_htg_vrt:*
       38:  em_sy:*
       39:  em_sy:*
       40:  em_hgo_hum:*
       40:  em_hgo_mus:*
       41:  em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result          Query
No.   Score   Match Length DB   ID                   Description
----- ------- ----- ------ ---- ----------------------------------------

No matches found

Search completed: June 23, 2004, 09:29:29
Job time : 6975 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: June 23, 2004, 07:21:45 ; Search time 4399 Seconds
(without alignments)
4514.287 Million cell updates/sec

Title: US-10-029-345A-109
Perfect score: 665
Sequence: 1 MAHEMIGTQIVTERLVALLE.........LGKVGSQSSFSGSSMEIIEVS 665

Scoring table:

| OLIGO | | | |
|-------|------|---------|------|
| Xgapop | 60.0 , | Xgapext | 60.0 |
| Ygapop | 60.0 , | Ygapext | 60.0 |
| Fgapop | 6.0 , | Fgapext | 7.0 |
| Delop | 6.0 , | Delext | 7.0 |

Searched: 27513289 seqs, 14931090276 residues

Word size: 1419

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US1029345/runat_23062004_072140_16043/app_query.fasta_1.839
-DB=EST -QFMT=fastap -SUFFIX=oli2.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=75
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US1029345 @CGN 1 1 3437 @runat_23062004_072140_16043 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_png:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| Result | | Query | | | |
|--------|-------|-------|------|-----|-------------|
| No. | Score | Match | Length | DB  ID | Description |
|--------|-------|-------|------|-----|-------------|

No matches found

Search completed: June 23, 2004, 10:42:56
Job time : 4399 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on:                June 23, 2004, 07:21:45 ; Search time 670 Seconds
                                                (without alignments)
                                                4216.495 Million cell updates/sec

Title:          US-10-029-345A-109
Perfect score:  665
Sequence:       1 MAHEMIGTQIVTERLVALLE.........LGKVGSQSSFSGGSMEIIEVS 665

Scoring table:  OLIGO
                Xgapop  60.0 ,  Xgapext  60.0
                Ygapop  60.0 ,  Ygapext  60.0
                Fgapop   6.0 ,  Fgapext   7.0
                Delop    6.0 ,  Delext    7.0

Searched:       3373863 seqs, 2124099041 residues

Word size:      1419

Total number of hits satisfying chosen parameters:  0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10029345/runat_23062004_072139_16024/app_query.fasta_1.839
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=oli2.rng -MINMATCH=0.1 -LOOPCL=0
-N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=oli2.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=75 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10029345 @CGN_1_1_470 @runat_23062004_072139_16024 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :      N_Geneseq_29Jan04:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002s:*
                7:  geneseqn2002as:*
                8:  geneseqn2003bs:*
                9:  geneseqn2003cs:*
                10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

                       %      Query
Result                 Score  Match  Length DB
No:     Score          Match  Length DB     ID     Description
------  -----          -----  ------ --     --     -----------

No matches found

Search completed: June 23, 2004, 07:33:06
Job time : 670 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on:        June 23, 2004, 07:21:50 ; Search time 1544 Seconds
                                          (without alignments)
                                          1973.073 Million cell updates/sec

Title:
Perfect score:    665
Sequence:         1 MAHEMIGTQIVTERLVALLE.........LGKVGSQSSFSGSMEIIEVS 665

Searched:         US-10-029-345A-109

Scoring table:
                  OLIGO
                  Xgapop  60.0  ;  Xgapext  60.0
                  Ygapop  60.0  ;  Ygapext  60.0
                  Fgapop   6.0  ,  Fgapext   7.0
                  Delop    6.0  ,  Delext    7.0

Searched:         3017426 seqs, 2290544650 residues

Word size:        1419

Total number of hits satisfying chosen parameters:    0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10029345/runat_23062004_072141_16083/app_query.fasta_1.839
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=o1i2.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=75 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1419
-ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10029345 @CGN 1 1 485 @runat 23062004 072141_16083
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :        Published_Applications NA:*
                  1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                  4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                  5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                  6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                  7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                  8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                  9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

--------------------------------------------------------------------

No matches found

Search completed: June 23, 2004, 11:11:03
Job time : 1545 secs

--------------------------------------------------------------------

SUMMARIES

Result    %       Query
No.    Score   Match  Length  DB    ID                          Description

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM protein - nucleic search, using frame_plus_p2n model

                          GenCore version 5.1.6
                          Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:          June 23, 2004, 07:21:50 ; Search time 125 Seconds
                                            (without alignments)
                                            2952.339 Million cell updates/sec

Title:
Perfect score:   US-10-029-345A-109
Sequence:        665
                 1 MAHEMIGTQIVTERLVALLE..........LGKVGSQSSFSGSMEIIEVS 665

Scoring table:

                 OLIGO
                 Xgapop   60.0  ,  Xgapext   60.0
                 Ygapop   60.0  ,  Ygapext   60.0
                 Fgapop    6.0  ,  Fgapext    7.0
                 Delop     6.0  ,  Delext     7.0

Searched:        682709 seqs, 277475446 residues

Word size:       1419

Total number of hits satisfying chosen parameters:      0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10029345//runat_23062004_072140_16059/app_query.fasta_1.839
-DB=Issued Patents NA. -QPMT=fastap -SUFFIX=oli2.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits  -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=75 -DOCALIGN=200  -THR_SCORE=quality -THR_MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto  -NORM=ext  -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10029345 @CGN_1_1_69 @runat_23062004_072140_16059 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :      Issued_Patents NA:*
                1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                        SUMMARIES

Result                  %         Query
No.      Score   Match Length DB   ID              Description
------   -----   ------------ ---  --              -----------

No matches found

Search completed: June 23, 2004, 10:45:09
Job time : 125 secs